STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/540,047_

Source: _Pu/10_

Date Processed by STIC: _6/30/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , **EFS Submission User Manual - ePAVE)**
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/540,047_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
        Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                             prevent "wrapping."

·2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
        Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                             ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                             each n or Xaa can only represent a single residue. Please present the maximum number of each
                             residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
        "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                             previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                             the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                             Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
        (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                             (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                             (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                             This sequence is intentionally skipped

                             Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
        (NEW RULES)   <210> sequence id number
                             <400> sequence id number
                             000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                             In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
         Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                             is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                             Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                             "Unknown." Please explain source of genetic material in <220> to <223> section.
                             (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
         "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                             listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid;

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/540,047

DATE: 06/30/2005
TIME: 09:05:27

Input Set : **A:\PTO.YF.txt**
Output Set: **N:\CRF4\06302005\J540047.raw**

```
     3 <110> APPLICANT: FUNDACION PARA LA INVESTIGACION CLINICA Y MOLECULAR
     4       DEL CANCER DE PULMON (LUNG CANCER CLINICAL AND MOLECULAR
     5       RESEARCH FOUNDATION)
W--> 6 <120> TITLE OF INVENTION: "ASSAY DEVICE OF XPD/ERCC2 GENE POLYMORPHISMS FOR THE
W--> 7       CORRECT ADMINISTRATION OF CHEMOTHERAPY IN LUNG CANCER"
W--> 8 <130> FILE REFERENCE: PCT-152
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/540,047
C--> 9 <141> CURRENT FILING DATE: 2005-06-22
W--> 9 <160> NUMBER OF SEQ ID: 8
```

see item 4 on Error Summary Sheet

ERRORED SEQUENCES

```
E--> 10 <210> SEQ ID NO: SEQ ID NO.:1
     11 <211> LENGTH: 15
E--> 12 <212> TYPE: oligonucleotide
     13 <213> ORGANISM: artificial sequence
W--> 14 <220> FEATURE:
W--> 15 <221> NAME/KEY: primer
W--> 16 <223> OTHER INFORMATION:
W--> 16 <400> SEQUENCE:
     17 acgcccacct ggcca         15
E--> 19 <210> SEQ ID NO: SEQ ID NO.: 2
     20 <211> LENGTH: 17
E--> 21 <212> TYPE: oligonucleotide
     22 <213> ORGANISM: artificial sequence
W--> 23 <220> FEATURE:
W--> 24 <221> NAME/KEY: primer
W--> 25 <223> OTHER INFORMATION:
W--> 25 <400> SEQUENCE:
     26 ggcgggaaag ggactgg         17
E--> 28 <210> SEQ ID NO: SEQ ID NO.: 3
     29 <211> LENGTH: 19
E--> 30 <212> TYPE: oligonucleotide
     31 <213> ORGANISM: artificial sequence
W--> 32 <220> FEATURE:
W--> 33 <221> NAME/KEY: primer
     34 <223> OTHER INFORMATION: TaqMan MGBTM VIC Probe
W--> 35 <400> SEQUENCE:
     36 ccgtgctgcc cgacgaagt         19
E--> 38 <210> SEQ ID NO: SEQ ID NO.: 4
     39 <211> LENGTH: 19
E--> 40 <212> TYPE: oligonucleotide
```
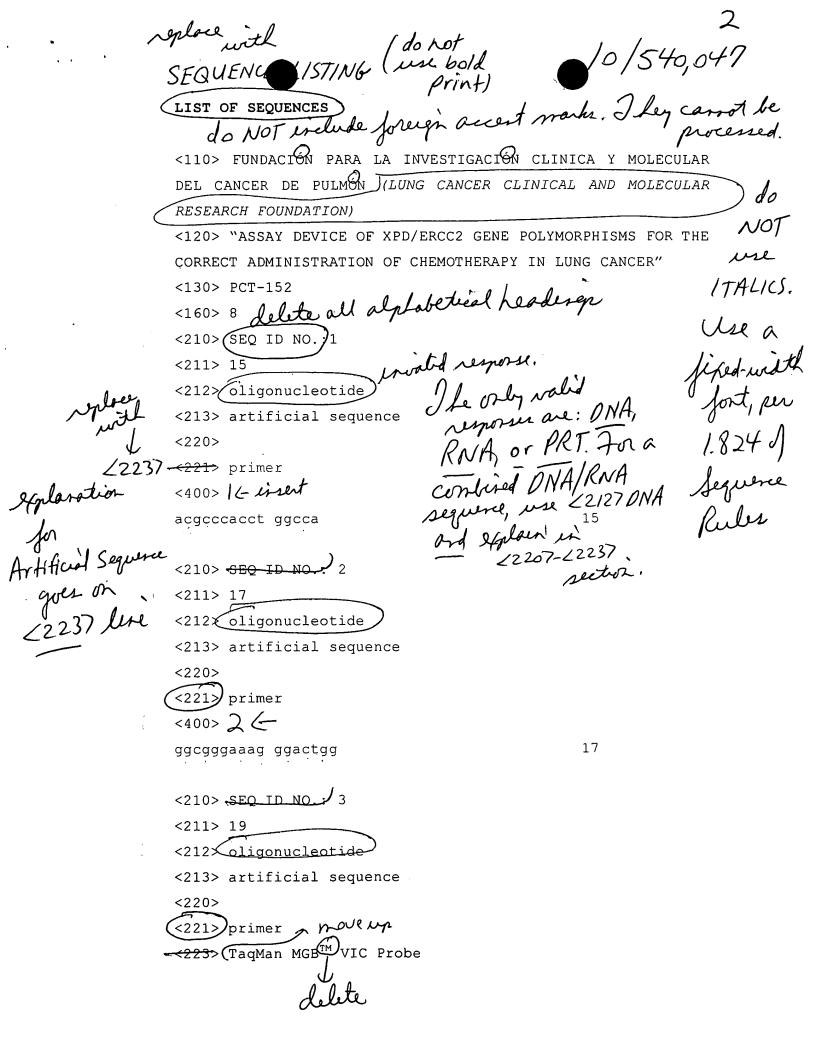
Does Not Comply Corrected Diskette Needed

See attached pages for error explanation.

Suggestion: consult Sequence Rules for valid format

replace with

SEQUENCE LISTING (do not use bold print)

2

10/540,047

do NOT include foreign accent marks. They cannot be processed.

<110> FUNDACION PARA LA INVESTIGACION CLINICA Y MOLECULAR DEL CANCER DE PULMON (LUNG CANCER CLINICAL AND MOLECULAR RESEARCH FOUNDATION)

do NOT use ITALICS.

<120> "ASSAY DEVICE OF XPD/ERCC2 GENE POLYMORPHISMS FOR THE CORRECT ADMINISTRATION OF CHEMOTHERAPY IN LUNG CANCER"

<130> PCT-152

<160> 8   delete all alphabetical headers

<210> SEQ ID NO. 1

<211> 15

<212> oligonucleotide   invalid response.

<213> artificial sequence

The only valid responses are: DNA, RNA or PRT. For a combined DNA/RNA sequence, use <212> DNA and explain in <220>-<223> section.

replace with
↓
<223> <221> primer

explanation for Artificial Sequence goes on <223> line

<400> 1 ← insert

acgcccacct ggcca

Use a fixed-width font, per 1.824 d) Sequence Rules

<210> SEQ ID NO. 2

<211> 17

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<400> 2 ←

ggcgggaaag ggactgg   17

<210> SEQ ID NO. 3

<211> 19

<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer ↗ move up

<223> TaqMan MGB™ VIC Probe

↓ delete

<400> 3

ccgtgctgcc cgacgaagt   19

<210> SEQ ID NO. 4
<211> 19
<212> oligonucleotide
<213> artificial sequence
<220>
<221> primer
<223> TaqMan MGB™ 6-FAM Probe
<400> 4

cccgtgctgc ccaacgaag   19

<210> SEQ ID NO. 5
<211> 22
<212> oligonucleotide
<213> artificial sequence
<220>
<221> primer
<400> 5

gcctggagca gctagaatca ga   22

<210> SEQ ID NO. 6
<211> 22
<212> oligonucleotide
<213> artificial sequence
<220>
<221> primer
<400> 6

cactcagagc tgctgagcaa tc   22

<210> SEQ ID NO. 7
<211> 16
<212> oligonucleotide

<213> artificial sequence

<220>

<221> primer

<223> TaqMan MGB™ VIC Probe

<400> 7

tatcctctgc agcgtc   16

<210> SEQ ID NO 8

<211> 17

<212> oligonucleotide

<213> artificial sequence

<220>

<223> <221> primer

<223> TaqMan MGB™ 6-FAM Probe

<400> 8

ctatcctctt cagcgtc   17